

## SEQUENCE LISTING

<110> BOUGERET, CECILE  
 ZARZOV, PATRICK  
 BRIAND, JEAN-FRANCOIS  
 THOMAS, DOMINIQUE

<120> METHOD FOR SCREENING AGENTS MODULATING I-KAPPA B-ALPHA  
 PROTEIN UBIQUITINATION AND MEANS FOR CARRYING OUT SAID  
 METHOD

<130> 0510-1149

<140> 10/592,944

<141> 2006-09-15

<150> PCT/FR05/050165

<151> 2005-03-15

<150> FR 04 50528

<151> 2004-03-16

<160> 26

<170> PatentIn Ver. 3.3

<210> 1

<211> 1719

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 construct

<400> 1

```

atgtctaaag gtgaagaatt attcactggt gttgtcccaa ttttggttga attagatggt 60
gatgttaatg gtcacaaatt ttctgtctcc ggtgaagggt aagggtgatgc tacttacggt 120
aaattgacct taaaatttat ttgtactact ggtaaattgc cagttccatg gccaacctta 180
gtcactactt tgggttatgg tgttcaatgt ttgtctagat acccagatca tatgaaacaa 240
catgactttt tcaagtctgc catgccagaa ggttatgttc aagaaagaac ttttttttc 300
aaagatgacg gtaactacaa gaccagagct gaagtcaagt ttgaagggtga taccttagtt 360
aatagaatcg aattaaaagg tattgatttt aaagaagatg gtaacatttt aggtcacaaa 420
ttggaataca actataactc tcacaatggt tacatcatgg ctgacaaaaca aaagaatggt 480
atcaaagtta acttcaaaat tagacacaac attgaagatg gttctgttca attagctgac 540
cattatcaac aaaataactc aattggtgat ggtccagtct tgttaccaga caaccattac 600
ttatccactc aatctgcctt atccaaagat ccaaacgaaa agagagacca catgggtcttg 660
ttagaatttg ttactgctgc tggattacc catgggtatgg atgaattgta caaactgcag 720
agcccacctc caaaaaagaa gagaaaggtc gaattgggag gatccatgtt ccaggcggcc 780
gagcgccccc aggagtgggc catggagggc cccgcgcacg ggctgaagaa ggagcggcta 840
ctggacgacc gccacgacag cggcctggac tccatgaaag acgaggagta cgagcagatg 900
gtcaaggagc tgcaggagat ccgcctcgag ccgcaggagg tgccgcgcgg ctccggagccc 960
tggaagcagc agctcacga ggaaggggac tcgttcctgc acttggccat catccatgaa 1020
gaaaaggcac tgaccatgga agtgatccgc cagggtgaagg gagacctggc tttcctcaac 1080
ttccagaaca acctgcagca gactccactc cacttggctg tgatcaccaa ccagccagaa 1140
attgctgagg cacttctggg agctggctgt gatcctgagc tccgagactt tcgaggaaat 1200
acccccctac accttgccctg tgagcagggc tgcctggcca gcgtgggagt cctgactcag 1260
tctctgcacca ccccgcacct ccactccatc ctgaaggcta ccaactacaa tggccacacg 1320

```

```

tgtctacact tagcctctat ccatggctac ctgggcatcg tggagctttt ggtgtccttg 1380
ggtgctgatg tcaatgctca ggagccctgt aatggccgga ctgcccttca cctgcgagtg 1440
gacctgcaaa atcctgacct ggtgtcactc ctgttgaagt gtggggctga tgtcaacaga 1500
gttacctacc agggctattc tccctaccag ctcacctggg gccgccaag caccggata 1560
cagcagcagc tgggcccagct gacactagaa aaccttcaga tgctgccaga gaggaggat 1620
gaggagagct atgacacaga gtcagagttc acggagttca cagaggacga gctgcctat 1680
gatgactgtg tgtttgaggg ccagcgtctg acgttatga 1719

```

<210> 2

<211> 572

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic construct

<400> 2

```

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1           5           10           15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
          20           25           30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35           40           45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50           55           60

Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln
 65           70           75           80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
          85           90           95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100           105           110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115           120           125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130           135           140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145           150           155           160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
          165           170           175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180           185           190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195           200           205

```

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val  
 210 215 220  
 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Leu Gln  
 225 230 235 240  
 Ser Pro Pro Pro Lys Lys Lys Arg Lys Val Glu Leu Gly Gly Ser Met  
 245 250 255  
 Phe Gln Ala Ala Glu Arg Pro Gln Glu Trp Ala Met Glu Gly Pro Arg  
 260 265 270  
 Asp Gly Leu Lys Lys Glu Arg Leu Leu Asp Asp Arg His Asp Ser Gly  
 275 280 285  
 Leu Asp Ser Met Lys Asp Glu Glu Tyr Glu Gln Met Val Lys Glu Leu  
 290 295 300  
 Gln Glu Ile Arg Leu Glu Pro Gln Glu Val Pro Arg Gly Ser Glu Pro  
 305 310 315 320  
 Trp Lys Gln Gln Leu Thr Glu Asp Gly Asp Ser Phe Leu His Leu Ala  
 325 330 335  
 Ile Ile His Glu Glu Lys Ala Leu Thr Met Glu Val Ile Arg Gln Val  
 340 345 350  
 Lys Gly Asp Leu Ala Phe Leu Asn Phe Gln Asn Asn Leu Gln Gln Thr  
 355 360 365  
 Pro Leu His Leu Ala Val Ile Thr Asn Gln Pro Glu Ile Ala Glu Ala  
 370 375 380  
 Leu Leu Gly Ala Gly Cys Asp Pro Glu Leu Arg Asp Phe Arg Gly Asn  
 385 390 395 400  
 Thr Pro Leu His Leu Ala Cys Glu Gln Gly Cys Leu Ala Ser Val Gly  
 405 410 415  
 Val Leu Thr Gln Ser Cys Thr Thr Pro His Leu His Ser Ile Leu Lys  
 420 425 430  
 Ala Thr Asn Tyr Asn Gly His Thr Cys Leu His Leu Ala Ser Ile His  
 435 440 445  
 Gly Tyr Leu Gly Ile Val Glu Leu Leu Val Ser Leu Gly Ala Asp Val  
 450 455 460  
 Asn Ala Gln Glu Pro Cys Asn Gly Arg Thr Ala Leu His Leu Ala Val  
 465 470 475 480  
 Asp Leu Gln Asn Pro Asp Leu Val Ser Leu Leu Leu Lys Cys Gly Ala  
 485 490 495  
 Asp Val Asn Arg Val Thr Tyr Gln Gly Tyr Ser Pro Tyr Gln Leu Thr  
 500 505 510

Trp Gly Arg Pro Ser Thr Arg Ile Gln Gln Gln Leu Gly Gln Leu Thr  
 515 520 525

Leu Glu Asn Leu Gln Met Leu Pro Glu Ser Glu Asp Glu Glu Ser Tyr  
 530 535 540

Asp Thr Glu Ser Glu Phe Thr Glu Phe Thr Glu Asp Glu Leu Pro Tyr  
 545 550 555 560

Asp Asp Cys Val Phe Gly Gly Gln Arg Leu Thr Leu  
 565 570

<210> 3

<211> 2583

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 construct

<400> 3

```

atgtctaaag gtgaagaatt attcactggt gttgtcccaa ttttggttga attagatggt 60
gatgttaatg gtcacaaatt ttctgtctcc ggtgaagggt aaggatgatc tacttacggt 120
aaattgacct taaaatttat ttgtactact ggtaaattgc cagttccatg gccaacctta 180
gtcactactt tcggttatgg tgttcaatgt tttgctagat acccagatca tatgaaacaa 240
catgactttt tcaagtctgc catgccagaa ggttatgttc aagaaagaac tatttttttc 300
aaagatgacg gtaactacaa gaccagagct gaagtcaagt ttgaagggtga taccttagtt 360
aatagaatcg aattaaaagg tattgatttt aaagaagatg gtaacatttt aggtcacaaa 420
ttggaataca actataactc tcacaatggt tacatcatgg ctgacaaaaca aaagaatggt 480
atcaaagtta acttcaaaat tagacacaaac attgaagatg gttctgttca attagctgac 540
cattatcaac aaaatactcc aattggtgat ggtccagtct tgttaccaga caaccattac 600
ttatccactc aatctgcctt atccaaagat ccaaacgaaa agagagacca catggtcttg 660
ttagaatttg ttactgctgc tgggtattacc catgggtatgg atgaattgta caaactgcag 720
agcccacctc caaaaaagaa gagaaagggt gaattgggag gatccatgga cccggccgag 780
gcggtgctgc aagagaaggc actcaagttt atgtgtctta tgcccagggt tctgtggctg 840
ggctgtctca gcctggcgga cagcatgcct tcgctgcgat gcctgtataa cccagggact 900
ggcgcaactc cagctttcca gaattcctca gagagagaag actgtaataa tggcgaaccc 960
cctaggaaga taataccaga gaagaattca cttagacaga catacaacag ctgtgccaga 1020
ctctgcttaa accaagaaac agtatgttta gcaagcactg ctatgaagac tgagaattgt 1080
gtggccaaaa caaaacttgc caatggcact tcagtatga ttgtgcccaa gcaacggaaa 1140
ctctcagcaa gctatgaaaa ggaaaaggaa ctgtgtgtca aatactttga gcagtgggtca 1200
gagtcagatc aagtgggaatt tgtggaacat ctatatccc aaatgtgtca ttaccaacat 1260
gggcacataa actcgtatct taaacctatg ttgcagagag atttcataac tgctctgcca 1320
gctcggggat tggatcatat tgctgagaac atctgtcat accctggatgc caaatcacta 1380
tgtgtgtctg aacttgtgtg caaggaaatg taaccgagtga cctctgatgg catgctgtgg 1440
aagaagctta tcgagagaat ggtcaggaca gaattctctgt ggagaggcct ggcagaacga 1500
agaggatggg gacagtattt attcaaaaac aaacctcctg acgggaatgc tcctcccaac 1560
tctttttata gagcacttta tcctaaaatt atacaagaca ttgagacaat agaatctaata 1620
tggagatgtg gaagacatag tttacagaga attcactgcc gaagtgaac aagcaaaagga 1680
gtttactgtt tacagtatga tgatcagaaa atagtaagcg gccttcgaga caacacaatc 1740
aagatctggg ataaaaacac attggaatgc aagcgaattc tcacaggcca tacaggttca 1800
gtcctctgtc tccagtatga tgagagagt atcataacag gatcatcgga ttccacgggtc 1860
agagtgtggg atgtaaatac aggtgaaatg ct aaacacgt tgattcacca ttgtgaagca 1920
gttctgcact tgcgtttcaa taatggcatg atggtagcct gctccaaaga tcgttccatt 1980
gctgtatggg atatggcctc cccaactgac at taccctcc ggagggtgct ggtcggacac 2040
cgagctgctg tcaatgttgt agactttgat ga caagtaca ttgtttctgc atctggggat 2100

```

```

agaactataa aggtatggaa cacaagtact tgtgaatttg taaggacctt aaatggacac 2160
aaacgaggca ttgcctgttt gcagtagcagg gacaggctgg tagtgagtgg ctcatctgac 2220
aacactatca gattatggga catagaatgt ggtgcatgtt tacgagtgtt agaaggccat 2280
gaggaattgg tgcgttgtat tcgatttgat aacaagagga tagtcagtgg ggcctatgat 2340
ggaaaaatta aagtgtggga tcttgtggct gctttggacc cccgtgctcc tgcagggaca 2400
ctctgtctac ggacccttgt ggagcattcc ggaagagttt ttcgactaca gtttgatgaa 2460
ttccagattg tcagtagttc acatgatgac acaatcctca tctgggactt cctaaatgat 2520
ccagctgccc aagctgaacc cccccgttcc ccttctcgaa catacaccta catctccaga 2580
tga

```

<210> 4

<211> 860

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic construct

<400> 4

```

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1           5           10           15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
      20           25           30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
      35           40           45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
      50           55           60

Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln
      65           70           75           80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
      85           90           95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
      100          105          110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
      115          120          125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
      130          135          140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
      145          150          155          160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
      165          170          175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
      180          185          190

```

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
 195 200 205  
 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val  
 210 215 220  
 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Leu Gln  
 225 230 235 240  
 Ser Pro Pro Pro Lys Lys Lys Arg Lys Val Glu Leu Gly Gly Ser Met  
 245 250 255  
 Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys Phe Met Cys  
 260 265 270  
 Ser Met Pro Arg Ser Leu Trp Leu Gly Cys Ser Ser Leu Ala Asp Ser  
 275 280 285  
 Met Pro Ser Leu Arg Cys Leu Tyr Asn Pro Gly Thr Gly Ala Leu Thr  
 290 295 300  
 Ala Phe Gln Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro  
 305 310 315 320  
 Pro Arg Lys Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn  
 325 330 335  
 Ser Cys Ala Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser  
 340 345 350  
 Thr Ala Met Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn  
 355 360 365  
 Gly Thr Ser Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser  
 370 375 380  
 Tyr Glu Lys Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser  
 385 390 395 400  
 Glu Ser Asp Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys  
 405 410 415  
 His Tyr Gln His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln  
 420 425 430  
 Arg Asp Phe Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala  
 435 440 445  
 Glu Asn Ile Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu  
 450 455 460  
 Leu Val Cys Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp  
 465 470 475 480  
 Lys Lys Leu Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly  
 485 490 495

Leu Ala Glu Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro  
 500 505 510  
 Pro Asp Gly Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro  
 515 520 525  
 Lys Ile Ile Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly  
 530 535 540  
 Arg His Ser Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly  
 545 550 555 560  
 Val Tyr Cys Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg  
 565 570 575  
 Asp Asn Thr Ile Lys Ile Trp Asp Lys Asn Thr Leu Glu Cys Lys Arg  
 580 585 590  
 Ile Leu Thr Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu  
 595 600 605  
 Arg Val Ile Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp  
 610 615 620  
 Val Asn Thr Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala  
 625 630 635 640  
 Val Leu His Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys  
 645 650 655  
 Asp Arg Ser Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr  
 660 665 670  
 Leu Arg Arg Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp  
 675 680 685  
 Phe Asp Asp Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys  
 690 695 700  
 Val Trp Asn Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His  
 705 710 715 720  
 Lys Arg Gly Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser  
 725 730 735  
 Gly Ser Ser Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala  
 740 745 750  
 Cys Leu Arg Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg  
 755 760 765  
 Phe Asp Asn Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys  
 770 775 780  
 Val Trp Asp Leu Val Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr  
 785 790 795 800

Leu Cys Leu Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu  
                   805                  810                  815

Gln Phe Asp Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile  
                   820                  825                  830

Leu Ile Trp Asp Phe Leu Asn Asp Pro Ala Ala Gln Ala Glu Pro Pro  
                   835                  840                  845

Arg Ser Pro Ser Arg Thr Tyr Thr Tyr Ile Ser Arg  
                   850                  855                  860

<210> 5  
 <211> 21  
 <212> DNA  
 <213> Simian virus 40

<400> 5  
 ccaaaaaaga agagaaaggt c

21

<210> 6  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 primer

<400> 6  
 gctgggtacc ttaataatca tattacatgg catta

35

<210> 7  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 primer

<400> 7  
 ggcggaattc tatagttttt tctccttgac gtta

34

<210> 8  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 primer



<400> 8  
 ggtcgggaatt catgtctaaa ggtgaagaat tattc 35

<210> 9  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic primer

<400> 9  
 ggcgggatcc gcccgggctc tgcagtttgt acaattcatc catacc 46

<210> 10  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic primer

<400> 10  
 ggcggcgggcc gccaccgagg tgggcgaatt tcttatgatt tatg 44

<210> 11  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic primer

<400> 11  
 ggcggagctc tggaagaacg attacaacag 30

<210> 12  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic primer

<400> 12  
 acctccaaaa aagaagagaa aggtcgaatt 30

<210> 13  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 primer

<400> 13  
 ggcgggtacc gtgagtaagg aaagagtgag g

31

<210> 14  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 primer

<400> 14  
 ggcggaattc tgttttatat ttgttgtaaa aag

33

<210> 15  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 primer

<400> 15  
 ggcggaattc atggactaca aagaccatga cgg

33

<210> 16  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 primer

<400> 16  
 ggcgggatcc gcccgggctc tgcagcttgt catcgtcac cttgta

46

<210> 17  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic peptide

&lt;400&gt; 17

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala  
1 5

&lt;210&gt; 18

&lt;211&gt; 8

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic peptide

&lt;400&gt; 18

Asp Tyr Lys Asp Asp Asp Asp Lys  
1 5

&lt;210&gt; 19

&lt;211&gt; 23

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic peptide

&lt;400&gt; 19

Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp  
1 5 10 15Tyr Lys Asp Asp Asp Asp Lys  
20

&lt;210&gt; 20

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic peptide

&lt;400&gt; 20

Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys Lys  
1 5 10 15

&lt;210&gt; 21

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic peptide

&lt;400&gt; 21

Met Asn Lys Ile Pro Ile Lys Asp Leu Leu Asn Pro Gln  
1 5 10

&lt;210&gt; 22

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic peptide

&lt;400&gt; 22

Val Arg Ile Leu Glu Ser Trp Phe Ala Lys Asn Ile Glu Asn Pro Lys  
1 5 10 15

Leu Asp Thr

&lt;210&gt; 23

&lt;211&gt; 74

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic peptide

&lt;400&gt; 23

Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu  
1 5 10 15Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu  
20 25 30Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro  
35 40 45Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu  
50 55 60Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg  
65 70

&lt;210&gt; 24

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 24

Pro Lys Lys Lys Arg Lys Val

1

5

<210> 25

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 25

acctcAAAA aagaagagaa aggtcgaatt

30

<210> 26

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 26

aattcgacct ttctcttctt ttttggaggt

30